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MicroRNAs govern immune responses to infectious agents, allergens, and autoantigens and function by posttranscriptional repression of their target genes. In this paper, we have addressed the role of microRNA-155 (miR-155) in the control of Helicobacter pylori infection of the gastrointestinal tract and the development of H. pylori-induced chronic gastritis and associated gastric preneoplastic pathology. We show that miR-155 is upregulated in the gastric mucosa of experimentally infected mice and that miR-155−/− mice fail to control H. pylori infection as a result of impaired pathogen-specific Th1 and Th17 responses. miR-155−/− mice are also less well protected against challenge infection after H. pylori-specific vaccination than their wild-type (wt) counterparts. As a consequence of their impaired T cell responses to H. pylori, miR-155−/− mice develop less severe infection-induced immunopathology manifesting as chronic atrophic gastritis, epithelial hyperplasia, and intestinal metaplasia. T cells from miR-155−/− mice that are activated by CD3/CD28 cross-linking expand less and produce less IFN-γ and IL-17 than wt T cells. Finally, we show in this paper using adoptive transfers that the phenotypes of miR-155−/− mice are likely due to T cell-intrinsic defects. In contrast to wt T cells, miR-155−/− T cells from infected donors do not control H. pylori infections in T cell-deficient recipients, do not differentiate into Th1 or Th17 cells, and do not cause immunopathology. In addition, naïve miR-155−/− T cells fail to induce chronic Th17-driven colitis in an adoptive transfer model. In conclusion, miR-155 expression is required for the Th17/Th1 differentiation that underlies immunity to H. pylori infection on the one hand and infection-associated immunopathology on the other. The Journal of Immunology, 2011, 187: 3578–3586.

MicroRNA-155 Is Essential for the T Cell-Mediated Control of Helicobacter pylori Infection and for the Induction of Chronic Gastritis and Colitis

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Abbreviations used in this article: BMDC, bone marrow-derived dendritic cell; DC, dendritic cell; DSS, dextran sulfate sodium; miR, microRNA; miRNA, microRNA; PMSS1, premouse Sydney strain 1; qRT-PCR, quantitative RT-PCR; snoR, small nucleolar RNA; SOCS1, suppressor of cytokine signaling 1; Treg, regulatory T cell; wild type; and W.T., wild type.

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Mi croRNAs (miRNAs) are an abundant class of small noncoding RNAs that modulate the expression of their target genes at the posttranscriptional level. They bind to the 3′ untranslated regions of specific target miRNAs, thereby suppressing their translation and promoting their degradation. Of the ~700 different miRNAs identified in the human genome to date, at least 100 are expressed in cells of the immune system. The development and function of innate as well as adaptive immune cell populations are now widely believed to be critically dependent on miRNA function (1). One miRNA in particular, miRNA (miR)-155, has received much attention because of its expression and activity in a variety of immune cell types, namely...
Th17 cells. *Helicobacter*-specific Th1 cells and their signature cytokine IFN-γ were further shown to be directly responsible for the induction of infection-associated preneoplastic pathology manifesting as chronic atrophic gastritis, epithelial hyperplasia, and intestinal metaplasia (18, 20). The adoptive transfer of IFN-γ-proficient but not −deficient T cells into TCRβ−/− mice was sufficient to eliminate the infection in the recipients and to induce the full range of preneoplastic pathology (18). Given the major contribution of T cells to the control of—and immunopathology induced by—*H. pylori*, as well as the crucial role of miR-155 in Th1 and Th17 responses, as determined in adoptive transfer experiments, 300,000 immunomagnetically sorted CD4+CD25− T cells or naive CD4+CD62L+CD44low T cells were further shown to be directly responsible for the infection in vitro and in patients (21, 22), we hypothesized that miR-155 should have a clearly discernible role in *H. pylori* pathogenesis. Indeed, we found that miR-155−/− mice were incapable of spontaneously controlling *H. pylori* and of developing vaccine-induced protective immunity and were consequently protected against infection-associated preneoplastic pathology. The phenotype of miR-155−/− mice could be attributed to a likely T cell-intrinsic defect and was corroborated by the inability of miR-155−/− T cells to proliferate and to produce IFN-γ and IL-17 upon activation via their TCR in vitro.

**Materials and Methods**

*Animal experimentation and H. pylori cultures*

C57BL/6, Rag1−/−, BL6, TCRβ−/−, and miR-155−/−BL6 (B6.Cg-Mir155tm1.1Rskyb/J) mice were purchased from The Jackson Laboratory (distributed by Charles River Laboratories, Sulzfeld, Germany). All strains were bred at a University of Zurich specific pathogen-free facility. Mice were maintained in individually ventilated cages and included in studies at 6 wk of age. All animal experimentation was conducted in accordance with cantonal and federal guidelines for the care and use of laboratory animals and was reviewed and approved by the Zurich cantonal veterinary office. Mice were orally immunized three times at weekly intervals with 1 mg *H. pylori* (strain SS1) sonicate advanuted with 10 μg cholera toxin (List Biologicals, Campbell, CA) and challenged 1 wk after the last immunization with autologous *H. pylori* by oral gavage of 10⁷ bacteria. For adoptive transfer experiments, 300,000 immunomagnetically sorted splenic CD4+CD25− T cells or naive CD4+CD62L+CD44low T cells (R&D Systems, Minneapolis, MN) were injected into the tail veins of Rag1−/− mice. Dextran sulfate sodium (DSS)-induced colitis was provoked by three cycles of 2% DSS administration in the drinking water (for 5 d) with 7-d compound-free intervals. The following Abs were used for FACS analysis: IFN-γ, IL-10, IL-17, IL-22, TNFα, IL-6, and IL-1β using the Leica Application Suite 3.3.0 software.

**Preparation of gastric/colonic tissue and single-cell suspensions; assessment of H. pylori colonization and histopathology**

Stomachs and colons were retrieved and dissected longitudinally into equally sized pieces. For quantitative assessment of *H. pylori* colonization, one section of each stomach was homogenized in *Brucella* broth, and serial dilutions were plated on horse blood plates for colony counting. For the quantitative assessment of gastric histopathology, Giemsa-stained sections according to the following published guidelines (25): grade 0, no changes observed; grade 1, minimal scattered mucosal inflammatory cell infiltrates, with or without minimal epithelial hyperplasia; grade 2, mild scattered to diffuse inflammatory cell infiltrates, sometimes extending into the submucosa and associated with erosions, with minimal to mild epithelial hyperplasia and minimal to mild

mucin depletion from goblet cells; grade 3, mild to moderate inflammatory cell infiltrates that were sometimes transmural, often associated with ulceration, with moderate epithelial hyperplasia and mucin depletion; grade 4, marked inflammatory cell infiltrates that were often transmural and associated with ulceration, with marked epithelial hyperplasia and mucin depletion; and grade 5, marked transmural inflammation with severe ulceration and loss of intestinal glands. Representative images were recorded at ×100 and ×200 final magnification with a Leica Leitz DM RB microscope equipped with a Leica DFC 420C camera. Images were acquired using the Leica Application Suite 3.3.0 software.

**Flow cytometry**

The following Abs were used for FACS analysis: IFN-γ-PE-Cy7, CD4-FITC (BD Biosciences CA), CD45-Pacific blue, and Ly6-G-allophycocyanin (all BioLegend, San Diego, CA). For intracellular IFN-γ staining, cells were restimulated and blocked for 5 h in medium containing 2.5 μg/ml brefeldin A (Invitrogen) in the presence of 10 ng/ml RlR-2 (R&D Systems). Bone marrow-derived DCs (BMDCs) were generated by culturing fresh wt bone marrow cells at a density of 50,000 per 96-well flat bottom in RPMI 1640 medium with 10% FCS and 4 ng/ml GM-CSF for 7 d. DCs were matured by addition of 500 ng/ml Escherichia coli LPS (Sigma-Aldrich) for 12 h. DCs and T cells were cocultured at a ratio of 1:2 (50,000 DCS/100,000 T cells) and 1 μg/ml anti-CD3e (BD Biosciences) and 10 ng/ml RlR-2. After 72 h of coculture, IFN-γ and IL-17 production were quantified by ELISA (R&D Systems) or IFN-γ-specific intracellular cytokine staining for FACS analysis (see flow cytometry). Proliferation was assessed by [3H]thymidine incorporation assay.

**Cytokine and miR-155 quantitative RT-PCR**

For quantitative RT-PCR (qRT-PCR) of IFN-γ and IL-17, RNA was isolated from scraped gastric mucosa (antrum and corpus) using a Nucleospin RNA II kit (Macherey-Nagel, Duren, Germany). Total RNA (1.5 μg) was used for cDNA synthesis with Superscript Reverse Transcriptase III (Life Technologies). The resulting cDNA served as a template for quantitative PCR performed with a LightCycler 480 using the SYBR Green I Master Mix (Roche, Basel, Switzerland). Absolute values of IFN-γ and IL-17 expression were normalized to the ΔΔCT method. Primer sequences were as follows: Tm 55˚C, 50 cycles—GAPDH, 5'-GAC ATT GTT GCC TCT TCC CAG TCA CCG-3' (forward) and 5'-CCC GTT GAT GAC CAG CTT CC-3' (reverse); and IL-17, 5'-CAT GCC TGT TTC TGT CTT CCA GAG CTG-3' (forward) and 5'-GTT GCT GAT GGC CTG ATT GTC TTT-3' (reverse); and IL-17, 5'-GCT CCA GAA GCC CCT CAG A-3' (forward) and 5'-AGC TTT CCC TCC GCA TGG A-3'. The qRT-PCR for miR-155 quantification was performed according to a two-step manufacturer’s protocol (Applied Biosystems) using specific primers for murine miR-155 (Assay-ID 001806) and small nucleolar RNA (snor)-202 (Assay-ID 001232) and 10 ng total RNA as template.

**Statistics**

GraphPad Prism 5.0 software (GraphPad, La Jolla, CA) was used for statistical analyses. All p values were calculated by Mann–Whitney U test unless otherwise indicated. Bonferroni–Holm corrections were made for multiple comparisons where appropriate. In all scatter plot graphs, the medians are indicated by horizontal bars. In column bar graphs, the SEM is indicated by vertical bars; n.s. stands for “not significant.”

**Results**

miR-155−/− mice fail to control experimental *H. pylori* infection because of their inability to generate Th1 and Th17 responses

Experimental murine *H. pylori* infections are controlled by MHC class II-restricted, Th1- and Th17-polarized Th cells (16, 18, 24). To examine a possible role for miR-155 in spontaneously reducing
*H. pylori* colonization upon experimental infection, wt and miR-155−/− mice were infected with the virulent *H. pylori* patient isolate PMSS1 for 1 and 2 mo and analyzed with respect to colonization, gastric cytokine levels, and gastric histopathology (Fig. 1). The expression of miR-155 was induced by ∼3-fold in the gastric mucosa of wt mice infected with *H. pylori* for 1 mo (Fig. 1A). miR-155−/− mice were colonized by at least 1 order of magnitude more densely than wt animals at both time points (Fig. 1B) and exhibited significantly lower levels of gastric IFN-γ and IL-17 production at 2 mo postinfection (Fig. 1C,1D). In line with

**FIGURE 1.** miR-155−/− mice are colonized more densely than wt controls, produce less IFN-γ and IL-17, and do not develop preneoplastic gastric pathology. A, wt C57BL/6 mice were infected for 1 mo with *H. pylori* PMSS1, and the gastric mucosal expression of miR-155 was assessed by quantitative PCR. miR-155 expression was normalized to snoR-202. B–G, C57BL/6 wt and miR-155−/− mice were infected for 1 or 2 mo with *H. pylori* PMSS1 as indicated. B, Gastric *H. pylori* colonization as determined by plating and colony counting. C and D, Gastric mucosal IFN-γ and IL-17 production as determined by qRT-PCR and normalized to GAPDH. The dotted line indicates the average baseline cytokine expression in uninfected controls of both genotypes (three to five mice each). E–G, Gastric histopathology at 1 mo (E, G) and 2 mo (F, G) postinfection. Scores in E and F were assigned independently for the parameters inflammation, atrophy, epithelial hyperplasia, and intestinal metaplasia. Representative micrographs of Giemsa-stained sections are shown in *G* at ×100 and ×200 final magnification in relation to uninfected controls of both genotypes. In A–F, each data point represents one mouse.
a role for both Th1 and Th17 cells in inducing *H. pylori*-associated gastric inflammation and gastric preneoplastic lesions, miR-155/−/− mice were almost completely protected against the histopathological changes manifesting as gastritis, gastric atrophy, epithelial hyperplasia, and intestinal metaplasia that are a hallmark of *H. pylori*-infected wt animals (Fig. 1E–G). In conclusion, miR-155 is crucially involved in the generation of Th1 and Th17 responses to experimental *H. pylori* infection, which control the infection on the one hand, and mediate infection-associated gastric immunopathology on the other.

miR-155/−/− mice are less well protected than wt mice upon *H. pylori*-specific vaccination and challenge

wt mice that receive three doses of an orally administered whole-cell *H. pylori* vaccine adjuvanted with cholera toxin develop protective immunity against challenge infection with the pathogen (16, 18). To assess whether miR-155/−/− mice are protected as well as wt mice, groups of both genotypes were vaccinated three times at weekly intervals prior to autologous challenge infection with the commonly used *H. pylori* vaccine strain SS1. Although both strains were able to reduce *H. pylori* burdens by ∼1 order of magnitude as a consequence of their prior immunization, the colonization levels in vaccinated miR-155/−/− mice were significantly higher than those of their vaccinated wt counterparts (Fig. 2A). The colonization levels of naive (nonvaccinated) mice showed a similar trend (Fig. 2A), reproducing the findings obtained by experimental infection with the virulent isolate PMSS1 (Fig. 1B). Vaccinated miR-155/−/− mice produced lower gastric levels of IFN-γ and IL-17 than vaccinated wt animals (Fig. 2B, 2C). Their gastric mucosal infiltration of CD45+ leukocytes, a reliable correlate of vaccine-induced protection (16), was significantly reduced compared with wt mice (Fig. 2D). As a consequence of their lower cytokine expression and leukocyte infiltration, miR-155/−/− mice exhibited less postchallenge gastritis than their vaccinated wt counterparts (Fig. 2E). In summary, miR-155 expression is essential for the optimal development of Th1/Th17-driven vaccine-induced protective immunity to *H. pylori* and contributes to the T cell-driven gastritis that is a hallmark of vaccinated, challenged wt mice.

miR-155/−/− T cells proliferate less and produce less IFN-γ and IL-17 than wt T cells upon activation in vitro

We and others (16–19) have shown that the spontaneous as well as the vaccine-induced control of *Helicobacter* infection depends on MHC class II-restricted, Th1- and Th17-polarized T cells. Speculating that the T cell-intrinsic expression of miR-155 is required to activate T cells and to generate IFN-γ– and/or IL-17–producing effector cells, we treated immunomagnetically purified CD4+ CD25− T cells with anti-CD3/anti-CD28 in vitro. In wt T cells, the expression of miR-155 was strongly induced upon anti-CD3/anti-CD28 treatment (Fig. 3A). miR-155/−/− T cells proliferated less than wt cells upon anti-CD3/anti-CD28 stimulation as determined by thymidine incorporation assay (Fig. 3B) and produced significantly less IFN-γ and IL-17 than miR-155-proficient T cells (Fig. 3C, 3D). In a complementary model, in which LPS-treated BMDCs provided costimulatory signals, miR-155/−/− T cells produced less IFN-γ than miR-155-proficient T cells as determined by ELISA and intracellular cytokine staining (Fig. 3E–G). IL-17 production was negligible under these circumstances (data not shown). Hypothesizing that regulatory T cells (Tregs) might also rely on miR-155 for proper function, we added immunomagnetically isolated CD4+CD25+ Tregs to the T cell

**FIGURE 2.** Vaccinated miR-155/−/− mice are less protected than their wt counterparts upon challenge infection with *H. pylori*. C57BL/6 wt and miR-155/−/− mice were vaccinated three times with *H. pylori* SS1 sonicate adjuvanted with cholera toxin prior to challenge infection with the autologous strain. All vaccinated, challenged mice were sacrificed along with naive but challenged controls at 2 wk postchallenge infection. *A*, Gastric *H. pylori* colonization as determined by plating and colony counting. *B* and *C*, Gastric mucosal IFN-γ and IL-17 production as determined by qRT-PCR and normalized to GAPDH. *D*, Gastric mucosal infiltration of CD45+ leukocytes, as determined by flow cytometric analysis of mucosal single-cell preparations. *E*, Inflammation scores as assigned to all mice included in the study. In *A*–*E*, each data point represents one mouse. i, infected; ii, immunized infected.
activation system shown in Fig. 3A–D. Both wt and miR-155+/− Tregs prevented the CD3/CD28 cross-linking–induced proliferation of T cells efficiently (Supplemental Fig. 1), indicating that miR-155 is not required for the suppressive activity of Tregs in vitro. Taken together, the results suggest that miR-155 is essential for the generation of Th1 and Th17 effector T cells subsets but dispensable for Treg function.

miR-155 is required for clearance of H. pylori and the induction of gastritis and gastric preneoplastic pathology in an adoptive T cell transfer model

We have shown earlier that the adoptive transfer of purified CD4+CD25− T cells from Helicobacter-infected donors is sufficient to induce infection-associated gastric preneoplastic pathology in T cell-deficient recipients (18, 24). The development of gastric immunopathology in this model is infection dependent on the part of the donor as well as the recipient (18). To examine a possible effect of miR-155 gene targeting in this model, we infected wt or miR-155+/− donors with H. pylori PMSS1 for 1 mo prior to the immunomagnetic isolation of splenic CD4+CD25− T cells. Rag-1−/− recipients were i.v. injected with either 300,000 wt or miR-155+/− T cells and were experimentally infected on the day of adoptive transfer. Rag-1−/− recipients of miR-155+/− T cells were significantly less capable of clearing the H. pylori infection than recipients of wt T cells (Fig. 4A) and produced lower levels of gastric IFN-γ and IL-17 (Fig. 4B,4C). Total leukocyte infiltration into the gastric mucosa was reduced in the recipients of miR-155+/− T cells (Fig. 4D), which also exhibited significantly less evidence of gastritis, atrophy, hyperplasia, and metaplasia than the recipients of wt T cells (Fig. 4E,4F). In summary, the results suggest that the deficiency of miR-155+/− mice in clearing experimental H. pylori infections and in generating vaccine-induced protective immunity is due to a T cell-intrinsic defect. The inability of miR-155+/− T cells to optimally produce IFN-γ or IL-17 upon in vitro activation (Fig. 3) lends further support to this model.

T cell-intrinsic expression of miR-155 is required for the induction of chronic inflammation in a T cell-driven model of colitis

Because of the mechanistic and molecular similarities between H. pylori-associated gastritis and T cell-driven models of chronic colitis, we hypothesized that miR-155+/− mice may be less able to induce chronic inflammation in a T cell-driven colitis model. We used a Rag-1−/−/−/− mouse model of colitis in which CD4+CD45R+CD45R0+CD45R-CD8+ T cell subsets are preferentially expanded (25). These mice are unable to clear colitis-inducing bacteria such as Citrobacter rodentium (25). We infected wt or miR-155+/− Rag-1−/−/−/− mice with C. rodentium and observed signs of colitis by histological analysis (Fig. 5A). Rag-1−/−/−/− miR-155+/− mice exhibited significantly less pathology (Fig. 5B) and were significantly less capable of clearing the C. rodentium infection (Fig. 5C) than Rag-1−/−/−/− wt controls. These results indicate that miR-155 is required for the development of chronic inflammation in a T cell-driven model of colitis.
inflammatory conditions of the colon, we hypothesized that the T cell-intrinsic expression of miR-155 should also influence disease outcome in murine colitis models. To test this notion, we adoptively transferred naive wt or miR-155<sup>−/−</sup>T cells into TCR<sup>−/−</sup> recipients and assessed the development of colitis symptoms 4 wk posttransfer (Fig. 5). The recipients of miR-155<sup>−/−</sup>T cells exhibited significantly lower colonic expression of IFN-γ and IL-17 than the recipients of wt T cells (Fig. 5A, 5B). The colonic mucosa of miR-155<sup>−/−</sup>T cell recipients was further infiltrated by substantially lower numbers of CD45<sup>+</sup> leukocytes, CD4<sup>+</sup> T cells, and Ly6G<sup>+</sup> neutrophils than their wt-recipient counterparts (Fig. 5C–E). The pathology scores of miR-155<sup>−/−</sup>T cell recipients—integrating the parameters inflammation, appearance of erosions and ulcerations, and epithelial hyperplasia—and intestinal metaplasia. In A–D and F, each data point represents one mouse.

**FIGURE 4.** miR-155<sup>−/−</sup>T cells fail to clear *H. pylori* and to induce gastric pathology upon adoptive transfer into Rag-1<sup>−/−</sup> recipients. Rag-1<sup>−/−</sup> mice were infected with *H. pylori* PMSS1 and i.v. injected with 300,000 splenic CD4<sup>+</sup>CD25<sup>−</sup>T cells isolated from *H. pylori*-infected wt or miR-155<sup>−/−</sup> donors. Recipients were sacrificed 1 mo postinfection/adoptive transfer. A, Gastric *H. pylori* colonization as determined by plating and colony counting. B and C, Gastric mucosal IFN-γ and IL-17 production as determined by qRT-PCR and normalized to GAPDH. The dotted line indicates the average baseline cytokine expression in uninfected controls that have not received cells. D, Gastric mucosal infiltration of CD45<sup>+</sup> leukocytes, as determined by flow cytometric analysis of mucosal single-cell preparations. E and F, Gastric histopathology as assessed on Giemsa-stained sections; representative micrographs are shown in E at ×100 and ×200 final magnification. Scores in F were assigned independently for the parameters inflammation, atrophy, epithelial hyperplasia, and intestinal metaplasia. In A–D and F, each data point represents one mouse.

Discussion

A role for miRNAs in immunity to bacterial infections was initially demonstrated in plants with the discovery that resistance of *Arabidopsis thaliana* to the pathogen *Pseudomonas syringae* depended on miR-393 (26). A first indication that mammalian miRNAs are required for the defense of mammalian cells and tissues against bacterial infectious agents was provided by the finding that
TLR4 ligands induce the NF-κB-dependent expression of miR-146a/b and miR-155 (2, 4, 6). miR-155−/− mice have since been shown to be hypersusceptible to *Salmonella typhimurium* infection and also cannot be vaccinated protectively against the pathogen (8), despite exhibiting no apparent immunological defects under steady-state conditions. The increased susceptibility of miR-155−/− mice to infectious agents has been attributed to their failure to generate proper Ab responses, which in turn may be due to defective class switching and plasma cell differentiation (7, 8). Additional immune deficiencies of miR-155−/− mice have been linked to DC-intrinsic defects and to imbalanced Th1/Th2 polarization (8). More recent reports using noninfectious disease models have confirmed an involvement of miR-155 in governing Th subset differentiation. Specifically, O’Connell et al. (11) showed that miR-155−/− mice are highly resistant to experimental autoimmune encephalomyelitis because of their defective development and function of Th17 cells.

miR-155 is strongly induced in various cell types upon coculture with *H. pylori* in vitro and is highly elevated in the gastric mucosa of chronically infected patients and of human volunteers experimentally infected with *H. pylori* (21, 22). In gastric epithelial cell lines, *H. pylori* was shown to induce miR-155 expression in an
NF-κB– and AP-1–dependent manner; in H. pylori-infected epithelial cells, overexpressed miR-155 appears to downregulate proinflammatory responses such as IL-8 production (22). T cells respond particularly strongly to H. pylori exposure (21). We confirm in this study using a model of virulent H. pylori infection that miR-155 expression is induced in the gastric mucosa of experimentally infected mice. Naive miR-155–deficient mice are incapable of controlling H. pylori and, as a consequence, are protected from the preneoplastic gastric immunopathology that is a hallmark of wt mice infected with virulent H. pylori (24). We attribute both the inability of the mice to restrict bacterial growth and their relative lack of pathology to strongly decreased gastric levels of IFN-γ and IL-17. Both cytokines are known to be required for H. pylori control and to contribute to gastric preneoplastic pathology (18–20). Interestingly, miR-155/−/− mice that have received several doses of an orally administered H. pylori vaccine are clearly better able than their nonvaccinated littermates to control a challenge infection. Nevertheless, colonization levels in vaccinated miR-155/−/− mice are significantly higher than in vaccinated wt mice, suggesting that optimal protective immunity requires miR-155. Again, decreased gastric levels of IFN-γ and IL-17 in the miR-155/−/− mice pointed to defective Th1 and Th17 differentiation and/or function. We propose that T cell intrinsic effects are responsible for the infection- and vaccination-associated phenotypes of miR-155/−/− mice, based on adoptive transfer experiments in which wt but not miR-155/−/− T cells effectively cleared the infection in the recipients and at the same time triggered gastric preneoplastic pathology.

Our observation that miR-155/−/− T cells proliferate less than wt cells and fail to produce IFN-γ or IL-17 upon CD3/CD28 cross-linking in vitro suggests that miR-155 regulates one or multiple pathways central to T cell activation. Among the targets identified for miR-155 in T cells are the Th1-promoting macrophage-activating factor c-MAF (8) and the negative regulator SOCS1 (5). SOCS1 functions downstream of cytokine receptors and participates in a negative feedback loop to attenuate cytokine signaling. The connection between miR-155 and SOCS1 was initially discovered in Tregs, which require the Foxp3-dependent expression of miR-155 for development (27) and competitive fitness (5). We did not detect a functional defect of miR-155/−/− Tregs in an in vitro suppression assay in this study, even though miR-155 is regulated by this Treg-specific transcription factor (21); moreover, the overall phenotype of the miR-155/−/− strain is more consistent with a dominant role for miR-155 in effecter T cells rather than Tregs in the context of H. pylori infection. Elucidating the T cell lineage-specific targets of miR-155 and the relative importance of these targets in Treg and effecter T cell functions remains a challenge for future work.

Our T cell adoptive transfer experiments designed to induce H. pylori infection-dependent gastritis and infection-independent colitis illustrate the strong defect of miR-155/−/− T cells in producing IFN-γ and IL-17 in vivo. The experiments further illustrate the mechanistic similarities of chronic inflammatory conditions of the stomach and lower gastrointestinal tracts, which in both cases are associated with T cellular production of IFN-γ and IL-17. In contrast to O’Connell et al. (11), we do not observe a differential defect in Th17 over Th1 cytokine production, because both cytokines are similarly reduced as a consequence of miR-155 gene deletion in our gastritis and colitis models. Rather, our data point toward a broader and more general role for miR-155 in Th cell differentiation and function. It will be interesting to examine in this context how miR-155/−/− mice behave in Th2-driven models of asthma and allergies. In conclusion, the T cell intrinsic expression of miR-155 is required for the Th1/Th17 cell differentiating and function that underlies immunity to H. pylori infection and elicits Helicobacter infection-associated immunopathology.

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Disclosures
The authors have no financial conflicts of interest.

References


Supplemental Figures

Suppl. Fig. 1:

Suppl. Fig. 1. *miR-155 is not required for the suppressive activity of Tregs* in vitro. Wild type and miR155<sup>−/−</sup> splenic CD<sup>4</sup><sup>+</sup>CD<sup>25</sup><sup>+</sup> T-cells were treated with anti-CD3/CD28-coated beads for 72 hours or left untreated. Wild type or miR155<sup>−/−</sup> splenic CD<sup>4</sup><sup>+</sup>CD<sup>25</sup><sup>+</sup> Tregs were added at a 2:1 (100,000 CD<sup>4</sup><sup>+</sup>CD<sup>25</sup><sup>+</sup> T-cells to 50,000 Tregs) or 1:1 ratio (100,000 CD<sup>4</sup><sup>+</sup>CD<sup>25</sup><sup>+</sup> T-cells to 100,000 Tregs) as indicated. The proliferation was determined by [³H] thymidine incorporation assay.
Suppl. Fig. 2. *miR-155^-/-* mice develop less severe colitis than wild type controls. *miR-155^-/-* and wild type animals were subjected to three cycles of DSS administration via the drinking water. *A,B*. Colonic mucosal IFN-γ and IL-17 production as determined by qRT-PCR, normalized to GAPDH. The dotted line indicates the average baseline cytokine expression in untreated controls. *C,D*. Colonic histopathology as assessed on Giemsa-stained sections; representative micrographs are shown in D at 100x and 200x final magnification. Scores in C were assigned on a scale of 0-5. In A-C, each data point represents one mouse.